

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:51:50 ; Search time 81.1136 Seconds
(without alignments)
659.727 Million cell updates/sec

Title: US-09-988-971-2_COPY_94_176

Perfect score: 446
Sequence: 1 WLYEGLSRKAEKLELLPGN.....WLYSRPLTPSLQALVDHY 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA Main:*

1: /cgn2_6/prodata/2/paa/US07_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US07_COMB.pep.*
3: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
4: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
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6: /cgn2_6/prodata/2/paa/US08_COMB.pep.*
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27: /cgn2_6/prodata/2/paa/US10_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446	100.0	149	27	US-60-208-965-212
2	446	100.0	149	27	US-60-213-178-695
3	446	100.0	197	21	US-09-791-537-122481
4	446	100.0	261	23	US-09-988-971-2
5	439	98.4	210	1	PCT-US01-42950-448
6	358	80.3	159	22	US-09-867-550-954

7	254	57.0	98	7	US-08-359-490-7	Sequence 7, Appl
8	254	57.0	98	8	US-08-475-031-7	Sequence 7, Appl
9	254	57.0	107	21	US-09-791-537-152868	Sequence 152868
10	254	57.0	383	21	US-09-791-537-116222	Sequence 116222
11	254	57.0	383	27	US-60-389-987-784	Sequence 784, App
12	254	57.0	383	27	US-60-412-418-784	Sequence 784, App
13	254	57.0	438	21	US-09-791-537-152929	Sequence 152929
14	254	57.0	454	21	US-09-791-537-152367	Sequence 152367
15	254	57.0	505	6	US-08-232-545-17	Sequence 17, Appl
16	254	57.0	505	21	US-09-791-537-193356	Sequence 193356
17	254	57.0	505	21	US-09-791-537-140287	Sequence 140287
18	254	57.0	505	23	US-09-977-260-17	Sequence 17, Appl
19	254	57.0	505	23	US-09-977-261-17	Sequence 17, Appl
20	254	57.0	505	23	US-09-977-269-17	Sequence 17, Appl
21	254	57.0	505	25	US-10-111-814-11	Sequence 11, Appl
22	254	57.0	526	21	US-09-791-537-140420	Sequence 140420
23	254	57.0	526	27	US-60-366-992-31	Sequence 31, Appl
24	246	55.2	488	21	US-09-791-537-91827	Sequence 91827, A
25	244	54.7	98	7	US-08-359-490-6	Sequence 6, Appl
26	244	54.7	98	8	US-08-475-031-6	Sequence 8, Appl
27	243	54.5	161	21	US-09-791-537-73855	Sequence 73855, A
28	243	54.5	276	21	US-09-791-537-12844	Sequence 12844, A
29	243	54.5	276	22	US-09-870-759-64	Sequence 64, Appl
30	243	54.5	276	23	US-09-988-971-6	Sequence 6, Appl
31	243	54.5	214	21	US-09-760-443-1254	Sequence 1254, Ap
32	243	54.5	314	21	US-09-760-446A-1268	Sequence 1268, Ap
33	243	54.5	314	21	US-09-760-446A-1282	Sequence 1282, Ap
34	243	54.5	314	26	US-10-206-664-1268	Sequence 1268, Ap
35	243	54.5	314	26	US-10-206-664-1282	Sequence 1282, Ap
36	243	54.5	314	26	US-10-212-054-1254	Sequence 1254, Ap
37	243	54.5	328	27	US-60-229-525-389	Sequence 389, App
38	242	54.3	512	21	US-09-791-537-132968	Sequence 132968
39	242	54.3	512	23	US-09-977-260-16	Sequence 16, Appl
40	242	54.3	512	23	US-09-977-261-16	Sequence 16, Appl
41	242	54.3	512	23	US-09-977-269-16	Sequence 16, Appl
42	242	54.3	512	23	US-09-977-269-16	Sequence 16, Appl
43	242	54.3	512	23	US-09-977-269-16	Sequence 16, Appl
44	242	54.3	512	23	US-09-977-269-16	Sequence 16, Appl
45	242	54.3	512	23	US-09-977-269-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-60-208-965-212
Sequence 212 Application US/60208965
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
FILE REFERENCE: CLO00639
CURRENT APPLICATION NUMBER: US/60/208,965
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 244
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 212
LENGTH: 149
TYPE: PRT
ORGANISM: HUMAN
US-60-208-965-212

Query Match 100.0%; Score 446; DB 27; Length 149;
Best Local Similarity 100.0%; Pred. No. 2, 7e-46;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WLYEGLSRKAEKLELLPGNCGAFILRSQRRSSYSLSVRLSPASMDRIHRIRHCL 60
66 WLYEGLSRKAEKLELLPGNCGAFILRSQRRSSYSLSVRLSPASMDRIHRIRHCL 125
QY 61 DWGWLISPLTPSLQALVDHY 83

Db 126 DNGWLYISPRLTFFPSLOALVDHY 148

RESULT 2

US-60-213-178-695
; Sequence 695, Application US/60213178
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1000689
; CURRENT APPLICATION NUMBER: US/60/213,178
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 1425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 695
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Human
US-60-213-178-695

Query Match

Best Local Similarity 100.0%; Score 446; DB 27; Length 149;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 60
Db 66 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 125

Qy 61 DNGWLYISPRLTFFPSLOALVDHY 83
Db 126 DNGWLYISPRLTFFPSLOALVDHY 148

RESULT 3

US-09-791-537-122481
; Sequence 122481, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomolx, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 122481
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-122481

Query Match 100.0%; Score 446; DB 21; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.8e-46;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 60
Db 30 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 112
Qy 61 DNGWLYISPRLTFFPSLOALVDHY 83
Db 90 DNGWLYISPRLTFFPSLOALVDHY 112

RESULT 4

US-09-988-971-2
; Sequence 2, Application US/09988971
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY

; TITLE OF INVENTION: CLONING AND EXPRESSION OF HUMAN SLAP-2: A NOVEL
; TITLE OF INVENTION: SH2/SH3 DOMAIN-CONTAINING HUMAN SLAP HOMOLOGUE HAVING
; FILE REFERENCE: D0043PCT
; CURRENT APPLICATION NUMBER: US/09/988,971
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252545
; PRIOR FILING DATE: 2000-11-22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-988-971-2

Query Match 100.0%; Score 446; DB 23; Length 261;
Best Local Similarity 100.0%; Pred. No. 5.4e-46;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 60
Db 94 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 153
Qy 61 DNGWLYISPRLTFFPSLOALVDHY 83
Db 154 DNGWLYISPRLTFFPSLOALVDHY 176

RESULT 5

PCT-US01-42950-448
; Sequence 448, Application PC/TUS0142950
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-096
; CURRENT APPLICATION NUMBER: PCT/US01/42950
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 09/714,936
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 448
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-42950-448

Query Match 98.4%; Score 439; DB 1; Length 210;
Best Local Similarity 98.8%; Pred. No. 3e-45;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 60
Db 94 WLYEGLSREKAEELLIPGNGAFLIRSGYSLSVRLSPASWDRIRHYRHCL 153
Qy 61 DNGWLYISPRLTFFPSLOALVDHY 83
Db 154 DNGWLYISPRLTFFPSLOALVDHY 176

RESULT 6

US-09-867-550-954
; Sequence 954, Application US/09867550
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Mehraban, Foad
; APPLICANT: Conley, Pamela
; APPLICANT: Law, Debbie
; APPLICANT: Topper, James
; TITLE OF INVENTION: Novel Polynucleotides from Atherogenic Cells and Polypeptides Enc
; FILE REFERENCE: 21402-013 (Cura-313)

CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 954
LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-954

Query Match 80.3%; Score 358; DB 22; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYEGLSREKAEELLPLPGNPGAFILRESQTRGSGSYSLVRLSPASMDRIRHRIHCL 60
DB 94 WYEGLSREKAEELLPLPGNPGAFILRESQTRGSGSYSLVRLSPASMDRIRHRIHCL 153
QY 61 DNGWLY 66
DB 154 DNGWLY 159

RESULT 7
US-08-359-490-7
Sequence 7, Application US/08359490

GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: Method for Assaying for a Substance that
Affects an SH2-Phosphorylated Ligand Regulatory System
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street, West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/359,490
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDiarmid, Shona S.
REGISTRATION NUMBER: P-38,798
REFERENCE/DOCKET NUMBER: 3153-135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-359-490-7

Query Match 57.0%; Score 254; DB 7; Length 98;
Best Local Similarity 57.8%; Pred. No. 8.6e-23;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
QY 1 WYEGLSREKAEELLPLPGNPGAFILRESQTRGSGSYSLVRLSPASMDRIRHRIHCL 60
DB 1 WYEGLSREKAEELLPLPGNPGAFILRESQTRGSGSYSLVRLSPASMDRIRHRIHCL 60

QY 61 DNGWLYSPRLTPPSLOALVDHY 83
DB 61 DNGWLYSPRLTPPSLOALVDHY 83

RESULT 8
US-08-475-031-7
Sequence 7, Application US/08475031

GENERAL INFORMATION:
APPLICANT: Pawson, Anthony
TITLE OF INVENTION: Method for Assaying for a Substance that
Affects an SH2-Phosphorylated Ligand Regulatory System
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street, West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,031
FILING DATE: June 6, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Linda M. Kurdzyk
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-475-031-7

Query Match 57.0%; Score 254; DB 8; Length 98;
Best Local Similarity 57.8%; Pred. No. 8.6e-23;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

QY 1 WYEGLSREKAEELLPLPGNPGAFILRESQTRGSGSYSLVRLSPASMDRIRHRIHCL 60
DB 1 WYEGLSREKAEELLPLPGNPGAFILRESQTRGSGSYSLVRLSPASMDRIRHRIHCL 60
QY 61 DNGWLYSPRLTPPSLOALVDHY 83
DB 61 DNGWLYSPRLTPPSLOALVDHY 83

RESULT 9

US-09-791-537-152868
Sequence 152868, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 152868

LENGTH: 107
TYPE: PRT
ORGANISM: pdb 3HCK
FEATURE:
NAME/KEY: misc:feature
LOCATION: (1)-(1)
OTHER INFORMATION: X is an unknown amino acid
US-09-791-537-152868

Query Match
Best Local Similarity 57.0%; Score 254; DB 21; Length 107;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGLSRKAEELLIPGNPGAFILRESQTRGSGYSLVRLSRPASMDRIHRYHCL 60
Db 6 WFFKGISRKDAERQLAPGNMGLSFMIRDETTKGSYSLSVRDYPDROGDTVHKYKIRTL 65
Qy 61 DNGMWLYISPRITFSPSLQALVDHY 83
Db 66 DNGGFYISPRSTFTLQELVDHY 88

RESULT 10
US-09-791-537-116222

Sequence 116222, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 116222
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-116222

Query Match
Best Local Similarity 57.0%; Score 254; DB 21; Length 383;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGLSRKAEELLIPGNPGAFILRESQTRGSGYSLVRLSRPASMDRIHRYHCL 60
Db 1 WFFKGISRKDAERQLAPGNMGLSFMIRDETTKGSYSLSVRDYPDROGDTVHKYKIRTL 60
Qy 61 DNGMWLYISPRITFSPSLQALVDHY 83
Db 61 DNGGFYISPRSTFTLQELVDHY 83

RESULT 11
US-60-389-987-784

Sequence 784, Application US/60389987
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088, 465P2
CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 784
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapiens
US-60-389-987-784

Query Match
Best Local Similarity 57.0%; Score 254; DB 27; Length 383;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGLSRKAEELLIPGNPGAFILRESQTRGSGYSLVRLSRPASMDRIHRYHCL 60
Db 1 WFFKGISRKDAERQLAPGNMGLSFMIRDETTKGSYSLSVRDYPDROGDTVHKYKIRTL 60
Qy 61 DNGMWLYISPRITFSPSLQALVDHY 83
Db 61 DNGGFYISPRSTFTLQELVDHY 83

RESULT 12
US-60-412-418-784

Sequence 784, Application US/60412418
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088, 465P3
CURRENT APPLICATION NUMBER: US/60/412,418
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 3025
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 784
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapiens
US-60-412-418-784

Query Match
Best Local Similarity 57.0%; Score 254; DB 27; Length 383;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGLSRKAEELLIPGNPGAFILRESQTRGSGYSLVRLSRPASMDRIHRYHCL 60
Db 1 WFFKGISRKDAERQLAPGNMGLSFMIRDETTKGSYSLSVRDYPDROGDTVHKYKIRTL 60
Qy 61 DNGMWLYISPRITFSPSLQALVDHY 83
Db 61 DNGGFYISPRSTFTLQELVDHY 83

RESULT 13
US-09-791-537-152929

Sequence 152929, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 152929
LENGTH: 438
TYPE: PRT

ORGANISM: pdb 1AD5A
FEATURE:
NAME/KEY: misc.feature
LOCATION: (434) (434)
OTHER INFORMATION: X is an unknown amino acid
US-09-791-537-152929

Query Match 57.0%; Score 254; DB 21; Length 438;
Best Local Similarity 57.8%; Pred. No. 5.4e-22;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGSRKAEELLPGNPGAFILRESQTRGSGYSLSVRLSRPASMDRIHRYHICL 60
Db 66 WFKGISRKDAEROLAPGNMLGSFMRDSEITTKGSYSLSVRYDPRQGDVTKHYKIRTL 125
Qy 61 DNGWLYISPRLTFFPSLQALVDHY 83
Db 126 DNGGFYISPRSTFTLQELVDHY 148

RESULT 14
US-09-791-537-152367

Sequence 152367, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biocomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patent version 3.0
SEQ ID NO 152367
LENGTH: 454
TYPE: PRT
ORGANISM: pdb 1QCPA
FEATURE:
NAME/KEY: misc.feature
LOCATION: (450) (450)
OTHER INFORMATION: X is an unknown amino acid
US-09-791-537-152367

Query Match 57.0%; Score 254; DB 21; Length 454;
Best Local Similarity 57.8%; Pred. No. 5.6e-22;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGSRKAEELLPGNPGAFILRESQTRGSGYSLSVRLSRPASMDRIHRYHICL 60
Db 72 WFKGISRKDAEROLAPGNMLGSFMRDSEITTKGSYSLSVRYDPRQGDVTKHYKIRTL 131
Qy 61 DNGWLYISPRLTFFPSLQALVDHY 83
Db 132 DNGGFYISPRSTFTLQELVDHY 154

RESULT 15
US-08-232-545-17

Sequence 17, Application US/08232545
GENERAL INFORMATION:
APPLICANT: Ulrich, Axel
APPLICANT: Gishizsky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-232-545-17

Query Match 57.0%; Score 254; DB 6; Length 505;
Best Local Similarity 57.8%; Pred. No. 6.4e-22;
Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;

Qy 1 WLYEGSRKAEELLPGNPGAFILRESQTRGSGYSLSVRLSRPASMDRIHRYHICL 60
Db 123 WFKGISRKDAEROLAPGNMLGSFMRDSEITTKGSYSLSVRYDPRQGDVTKHYKIRTL 182
Qy 61 DNGWLYISPRLTFFPSLQALVDHY 83
Db 183 DNGGFYISPRSTFTLQELVDHY 205

Search completed: March 24, 2003, 16:03:25
Job time: 82.3636 secs

